REMARKS

UNITY OF INVENTION

The examiner requires restriction under 35 USC §§121 and 372, alleging that the defined groups lack unity of invention as defined in PCT Rule 13.1. It is the examiner's argument that these groups lack unity of invention based on the different combinations of DNA sequences and on the difference between a process of transformation and a gene construct. Applicants provisionally elect Group I as defined by the examiner and traverse the restriction requirement.

Unity of invention is proper where a group of inventions share one or more of the same or corresponding special technical features, i.e., those technical features which define a contribution which each invention, considered as a whole, makes over the prior art. PCT Rule 13.2. The examiner's articulation of the present technical features omits the clearly unifying concept at the heart of the present claims. Each defined group, other than Group VII, contains reference to a combination of the S-adenosylmethionine (SAM) synthase gene and one of three identified biotin synthesis genes (bioS1, bioS2, and bioS3). Coexpression of the SAM synthase gene with one or more of the biotin synthesis genes is a technical feature "defin[ing] a contribution which each invention, considered as a whole, makes over the prior art." *Id.*

Accordingly, as each group shares this special technical feature, unity of invention is present and restriction is improper. Applicants respectfully request that the restriction requirement be withdrawn.

SEQUENCE LISTING

In response to the notice to comply with requirements for patent applications containing nucleotide sequence and/or amino acid sequence disclosures, a copy of the substitute sequence listing in computer readable form is attached hereto. The content of the paper copy of the sequence listing and the copy of the sequence listing in computer readable form is the same, and includes no new matter.

The above amendments to the specification include an updated Sequence Listing with current information pertinent to the present application. This information includes the names of the proper applicants, the serial number and filing date of the present application and the application number and filing date of the corresponding international application. The substitute sheets of the Sequence Listing also contain 2 sequences that are found in the body of the specification which were not included in the originally filed Sequence Listing.

Sequence numbers 16 and 17 are found in the original specification at page 13, and the origin of these sequences is described on that page, as well. The original specification has also been amended to include the sequence identification numbers where these are appropriate to aid in the identification of the amino acid and nucleic acid sequences to which reference is made.

Applicants respectfully assert that the amendments to the specification as a whole, and to the substitute Sequence Listing in particular, contain no new matter. It is

believed that by submitting the present amendment and the sequence listing diskette, the application now fully complies with the requirements of 37 CFR §§ 1.821-1.825. Applicants respectfully solicit issuance of the patent.

CONCLUSION

In view of the foregoing amendments and remarks, applicants consider that the rejections of record have been obviated and respectfully solicit passage of the application to issue.

Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 11-0345. Please credit any excess fees to such deposit account.

Respectfully submitted,
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AMENDMENTS

IN THE SPECIFICATION

Please amend the paragraph found on lines 14 to 21 of page 13 as follows:

metK was to be amplified as an expression cassette which was composed of a ribosome binding site, the start codon of the coding sequence and the stop codon between two restriction enzyme recognition sites. The Acc65I recognition sequence was chosen for both the restriction sites. The metK gene was amplified and cloned using the nucleotides PmetK1 ~~(5'- GCGGTACCAGGTGATATTAAATATGGCAAAAC-3')~~ (5'-gcggtaccag gtgatattaa atatggcaaa ac-3') (SEQ ID NO:16) and PmetK2 ~~(5'-CGGGTACCGATTACTTCAGACCGGCAGC-3')~~ (5'-cgggtaccga ttacttcaga ccggcagc-3') (SEQ ID NO:17).

Please replace the originally filed sequence listing with the sequence listing appended hereto and numbered separately as pages 1 to 36.